# Emma Dann

# Education

**PhD in Biological Sciences** – University of Cambridge, UK (Oct 2019 – Oct 2023) Advisors: Dr. Sarah A. Teichmann, Dr. John C. Marioni Thesis title: *Discovering variation from cell atlases: comparative methods for single-cell genomics* 

**M.Sc. in Cancer, Stem Cells and Developmental Biology (Bioinformatics profile)** – Utrecht University, NL (Sept 2017 – Aug 2019) Final grade: *cum laude* (Honours, Avg. grade: 9.10/10)

**B.Sc. in Biomolecular Sciences and Technology** – University of Trento, IT (Sept 2014 – July 2017) Final grade: 110 *cum laude*/110 (Avg. grade: 29.58/30)

# Professional experience

**Post-doctoral fellow – Stanford University, Palo Alto, USA** (May 2024 – present) Hosted by Jonathan Pritchard and Alex Marson (visiting fellow at Gladstone Institutes)

**Core team member – scverse consortium** (Feb 2024 – present) Community and teaching

**Data science consultant – Ensocell Ltd** (Oct 2023 – Mar 2024) Target discovery platform and analysis of single-cell data

**Graduate researcher – Wellcome Sanger Institute, Cambridge, UK** (Oct 2019 – Jan 2024) Supervised by Sarah Teichmann and John Marioni. Statistical methods for comparative analysis of single-cell omics data.

**Research intern – European Molecular Biology Laboratory, Heidelberg, DE** (Sept 2018 – Aug 2019) Supervised by Wolfgang Huber. Integrative analysis of multi-omic profiles of perturbations for functional characterization of drug treatments and target discovery.

**Research intern – KNAW Hubrecht Institute, Utrecht, NL** (Sept 2017 – Aug 2018) Supervised by Alexander Van Ourdenaarden. Biophysical modelling of whole-genome amplification via random priming, to predict and enhance coverage of single-cell bisulfite sequencing experiments.

**Research intern – Center for Integrative Biology, University of Trento, IT** (Feb 2017 – July 2017) Supervised by Francesca Demichelis. Computational analysis of whole-methylome profiles of tumor samples from a large cohort of prostate cancer patients, for epigenetic biomarker discovery.

**Research assistant – Center for Integrative Biology, University of Trento, IT** (Feb 2016 – Feb 2017) Lab equipment maintenance and general support for benchwork.

# Publications

(\*) denotes equal contribution as co-first author

#### Journal articles

Barnes J. L., He P., ..., **Dann E.**, ..., Teichmann S.A., Meyer K. B., Nikolic M. Z. (2022) Early human lung immune cell development and its role in epithelial cell fate. *Science Immunology* | Full text

**Dann E.**, Cujba A.M., Oliver A., Meyer K., Teichmann S.A., Marioni J.C. (2023) Precise identification of cell states altered in disease with healthy single-cell references, *Nature Genetics* | Full text | code | python package

Botting R.A., Goh I., ... , **Dann E.**, ... , Teichmann S.A. , Haniffa M. (2023) Yolk sac cell atlas reveals multiorgan functions during human early development. *Science* | Full text

Suo C., Polanski K., **Dann E.**, ..., Tuong Z.K., Clatworthy M., Teichmann S.A. (2023) Dandelion uses the single-cell adaptive immune receptor repertoire to explore lymphocyte developmental origins, *Nature Biotechnology* | Full text | python package

Heumos L., ... Single-cell Best Practices Consortium, ..., Theis F.J. (2023) Best practices for single-cell analysis across modalities. *Nature Review Genetics* | Full text

Suo C.\*, **Dann E.**\*, ... , Haniffa M., Teichmann S.A. (2022) Mapping the developing human immune system across organs. *Science* | Full text | code | data

He P., Lim K., Sun D., ..., **Dann E.**, ..., Meyer K.B., Rawlins E.L. (2022) A human fetal lung cell atlas uncovers proximal-distal gradients of differentiation and key regulators of epithelial fates, *Cell* | Full text

Kleshchevnikov V., Shmatko A., **Dann E.**, ..., Stegle O., Bayraktar O.A. (2022) Cell2location maps fine-grained cell types in spatial transcriptomics. *Nature Biotechnology* | Full text | python package

**Dann E.**, Henderson N.C., Teichmann S.A., Morgan M.D., Marioni J.C. (2022) Differential abundance testing on single-cell data using k-nearest neighbor graphs, *Nature Biotechnology* | Full text | R package | python package

Jardine L., Webb S., ... , **Dann E.**, ... , Göttgens B., Roberts I., Teichmann S. and Haniffa M. (2021) Blood and immune development in human fetal bone marrow and Down syndrome, *Nature* I Full text

Elmentaite R., Kumasaka N., Roberts K., Fleming A., **Dann E.**, ..., James K.R., Teichmann S.A. (2021), Cells of the human intestinal tract mapped across space and time, *Nature* I Full text

Stephenson E., Reynolds G., Botting R.A., Calero-Nieto F.J., Morgan M.D., Tuong Z.K., Bach K., Sungnak W., ..., **Dann E.**, ..., Duncan C.J.A, Smith K., Teichmann S.A., Clatworthy M.R., Marioni J.C., Gottgens B., Haniffa M. (2020) Single-cell multi-omics analysis of the immune response in COVID-19, *Nature Medicine* | Full text

Beltran H., Romanel A., ..., **Dann E.**, ..., Benelli M., and Demichelis F. (2020) Circulating Tumor DNA Profile Recognizes Transformation to Castration-Resistant Neuroendocrine Prostate Cancer, *Journal of Clinical Investigation* | Full text

#### **Conference** papers

Lalchand V.\*, Ravuri A.\*, **Dann E.**\*, ..., Teichmann S.A., Lawrence N.D. (2022) Modelling Technical and Biological Effects in scRNA-seq data with Scalable GPLVMs. *Proceedings of the 17th Machine Learning in Computational Biology meeting* | Full text

#### **Pre-prints**

Yayon N., Kedlian V., ..., **Dann E.**, ..., Teichmann S.A. (2023) A spatial human thymus cell atlas mapped to a continuous tissue axis. *biorXiv* | Full text

Schuster V., **Dann E.**, Krogh A., Teichmann S.A. (2023) multiDGD: A versatile deep generative model for multi-omics data. *biorXiv* | Full text | python package

Sumanaweera D., Suo C., Muraro D., **Dann E.**, ..., Teichmann S.A. (2023) Gene-level alignment of single cell trajectories informs the progression of in vitro T cell differentiation. *biorXiv* | Full text | python package

Missarova A., **Dann E.**, ... , J.C. Marioni (2023) Sensitive cluster-free differential expression testing. *biorXiv* | Full text | R package

### Software

**miloR** | **O** MarioniLab/miloR | primary developer | R/Bioconductor package for the identification of differential cell abundance in KNN graphs for single-cell data

**milopy** | **O** emdann/milopy | primary developer | python package for the identification of differential cell abundance in KNN graphs for single-cell data

**oor\_benchmark** | **O** MarioniLab/oor\_benchmark | primary developer | python framework to benchmark workflows for detection of out-of-reference cells in comparative single-cell analysis

**genomic-features** | **O** scverse/genomic-features | primary developer | Genomic annotations using Bioconductor resources in Python.

scverse-tutorials | 🖓 scverse/scverse-tutorials | contributor | tutorials for single-cell omics data analysis in python

single-cell-best-practices | O theislab/single-cell-best-practices | contributor | open source book on best practices for single-cell genomics data analysis

cell2location | PayraktarLab/cell2location | contributor | python package for mapping of tissue cell types via integration of single cell RNA-seq and spatial transcriptomics data

### Presentations

#### **Conference oral presentations**

Nov 2022 - Machine Learning in Computational Biology conference, virtual June 2022 - Single Cell Biology conference, Wellcome Genome Campus, Hinxton (UK) May 2022 - The Biology of Genomes, Cold Spring Harbor Laboratory (US) Oct 2021 - Chan Zuckerberg Initiative Single Cell Biology Meeting, virtual Sept 2021 - Next Generation Genomics Meeting, virtual Mar 2021 - CZI Seed Networks Computational biology meeting, virtual

#### **Invited** seminars

Mar 2024 - Human Technopole, Milan (IT) Dec 2023 - Google DeepMind, London (UK) Aug 2023 - University of Sri Jayewardenepura single-cell genomics seminar series, virtual Jul 2023 - Sanofi Precision Medicine & Computational biology, Cambridge (US) Jun 2023 - Chan Zuckerberg Initiative, Redwood City (US) Apr 2023 - Cambridge AI club for biomedicine, Milner Institute, Cambridge (UK) Dec 2022 - UMC Utrecht single-cell genomics meeting, virtual Sept 2022 - UK Conference of Bioinformatics and Computational Biology, virtual Jul 2022 - Computational Health Center seminar, Helmholtz Munich (DE) Apr 2022 - Maxwell Society Annual Conference, King's College London (UK) Apr 2022 - NYU Langone single cell journal club, virtual Mar 2021 - Cambridge Center for Physical Biology Single Cell Symposium, virtual

#### **Conference poster presentations**

July 2023 - Human Cell Atlas General Meeting, Toronto (CA) Oct 2022 - Single Cell Genomics conference, Utrecht (NL) Jun 2021 - Human Cell Atlas General Meeting, virtual

#### Lab meetings

Aug 2023 - Marson lab @ Gladstone Institutes

Jun 2023 - Shalek lab @ Broad institute of MIT and Harvard

Jun 2023 - Ye lab @ UCSF

May 2023 - Pritchard lab @ Stanford Genetics

Jan 2023 - Theis lab @ ICB Helmholtz Munich

May 2022 - Pe'er lab @ Memorial Sloan Kettering Cancer Center

May 2022 - Satija lab @ New York Genome Center

Apr 2022 - Lawrence group @ Computer laboratory, University of Cambridge

#### Other meetings and events

Apr 2023 - Scverse community hackathon on software interoperability, Heidelberg (DE) Dec 2022 - Scverse community hackathon on documentation, Innsbruck (AT) Apr 2021 - Open Problems in Single-Cell Analysis Jamboree, virtual

# Teaching & mentoring experience

Mar 2023 - Introduction to multiomics data integration and visualisation (EMBL-EBI training course) – Instructor for data integration case study

Jul 2022 - Systems biology: From large datasets to biological insight (EMBL-EBI training course) – Instructor for single-cell multi-omics module

Apr 2022 - Advanced topics in Single Cell Genomics (Swiss Institute for Bioinformatics course) – Trainer for multiomics module

Aug 2021 - Advanced topics in Single Cell Genomics (SciLifeLab / Swiss Institute for Bioinformatics Summer School) – Trainer for multi-omics project

Fall 2021 - PhD rotation student recruitment and mentoring, Teichmann lab

# Fellowships & awards

Oct 2019 - Wellcome Sanger Institute PhD studentship (Wellcome Trust, UK)

Jan 2018 - U/Select honours programme and travel grant (Utrecht University, NL)

Oct 2017 - Merit Award for excellent graduates (University of Trento, IT)

## Professional service

#### Conference/workshop organization

Nov 2023 - Scverse hackathon on multi-condition analysis tools, Cambridge (UK) - main organizer

Fall 2023 - Open Problems Single-cell perturbations Kaggle competition - member of judge panel

Apr 2021 - Open Problems in Single-Cell Analysis Jamboree - co-organizer

Feb 2020 - EBI-Sanger-Cambridge PhD Symposium - member of the organizing committee

#### Outreach

Sanger prize competition - member of the selection panel (Mar 2023) The Sanger Prize competition funds research internships at Sanger for undergraduate students from LMI countries. I've volunteered as a member of the Grad Panel, evaluating essays from applicants.

Open Wet Lab (OWL) - board member (Oct 2015 – Jan 2018) OWL is the first biohacking organization in Italy. I was in charge of the association's budget and directed the publication of OWL's blog and scientific outreach articles for local newspapers.

#### **Peer review**

Nature Biotechnology (2\* papers) Cell (1\* paper) OUP Bioinformatics (1 paper) Bioinformatics Advances (1 paper) Machine Learning in Computational Biology (MLCB) \*Assisting a senior reviewer